

Art Unit: 1652

APPENDIX A

US-09-746-491-21

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; Sequence 21, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20020137202A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-746-491-21
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Alignment Scores:

Pred. No.:	4.05e-127	Length:	1216
Score:	1051.00	Matches:	212
Percent Similarity:	68.39%	Conservative:	0
Best Local Similarity:	68.39%	Mismatches:	0
Query Match:	94.68%	Indels:	98
DB:	9	Gaps:	1

US-10-074-978A-24 (1-212) x US-09-746-491-21 (1-1216)

Qy	1 ValGlyAlaAlaValPheAspAlaLeuGluSerGluAlaGluSerGlyArgGlnArgLeu	20
Db		120
Qy	21 LeuValGlnLysArgGlyAlaLeuArgArgLysPheGlyPheSerAlaGluAspTyrArg	40
Db	121 CTGGTCCAGAACGGGGCGCTCTCCGAGGAAGTCGGCTTCTCGGCCGAGGACTACCGC	180
Qy	41 GluLeuGluArgLeuAlaLeuGlnAlaGluProHisArgAlaGlyArgGlnTrpLysPhe	60
Db	181 GAGCTGGAGCGCCTGGCGCTCCAGGCTGAGCCCCACCGCGCCGCCAGTGGAAAGTTC	240
Qy	61 ProGlySerPheTyrPheAlaIleThrValIleThrIleGluTyrGlyHisAlaAla	80
Db	241 CCCGGCTCTTCACTTCGGCATCACGTCACTACCACATCGAGTACGGCACGCCGCG	300
Qy	81 ProGlyThrAspSerGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeu	100
Db	301 CCGGGTACGGACTCCGGCAAGGTCTTCTGCATGTTCTACGGCTCCTGGCATCCGCTG	360
Qy	101 ThrLeuValThrPheGlnSerLeuGlyGluArgLeuAsnAlaValValArgArgLeuLeu	120
Db	361 ACGCTGGTCACTTCCAGAGCCTGGCGAACGGCTGAACGCCGGTGGTGCAGCGCTCCTG	420
Qy	121 LeuAlaAlaLysCysCysLeuGlyLeuArgTrpThrCysValSerThrGluAsnLeuVal	140
Db	421 TTGGCGGCCAAGTGCTGCCTGGCCCTGGGTGGACGTGCGTGTCCACGGAGAACCTGGTG	480
Qy	141 ValAlaGlyLeuLeuAlaCysAlaAlaThrLeuAlaLeuGlyAlaValAlaPheSerHis	160
Db	481 GTGGCCGGCTGCTGGCGTGTGCCACCCCTGGCCCTGGGGCCGTGCCCTCTCGCAC	540
Qy	161 PheGluGlyTrpThrPhePheHisAlaTyrTyrCysPheIleThrLeuThrThrIle	180
Db	541 TTCGAGGGCTGGACCTTCTCCACGCCTACTACTGCTTCACTCACCCCTCACCACCATC	600
Qy	181 GlyPheGly-----	183

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Db 601 GGCTTCGGCGACTTCGTGGCACTGCAGAGCGCGAGGCGCTGCAGAGGAAGCTCCCTAC 660
Qy 183 ----- 183
Db 661 GTGGCCTTCAGCTTCCCTACATCCTCCTGGGCTACGGCATGGCGCTTCCTAAC 720
Qy 183 ----- 183
Db 721 CTGGTGGTCCCTGCGCTTCCCTCGTTGCCAGCGCCGACTGGCCCGAGCGCGCTGCCGCACC 780
Qy 183 ----- 183
Db 781 CCCAGCCCCGCCCGGGGGCGCCCGAGAGCCGTGGCCTCTGGCTGCCCGCCGCCCG 840
Qy 183 ----- 183
Db 841 GCCCGCTCCGTGGCTCCGCCTGTCTCTGCCACGTGCACAAGCTGGAGAGGTGCC 900
Qy 184 ---AspAsnLeuGlyPheSerProProSerSerProGlyValValArgGlyGlyGlnAla 202
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Db 901 CGCGACAAACCTGGGCTTTGCCCGCCCTCGAGCCGGGGTCGTGCGTGGCGGCAGGCT 960
Qy 203 ProArgLeuGlyAlaArgTrpLysSerIle 212
||| ||| ||| ||| ||| ||| |||
Db 961 CCCAGGCTTGGGGCCCGTGGAAAGTCCATC 990